In the Specification

On page 7, please replace the paragraph at line 12 with the following:

As used herein, the designation of a particular polymorphism is made by the name of a particular restriction enzyme. This is not intended to imply that the only way that the site can be identified is by the use of that restriction enzyme. There are numerous databases and resources available to those of skill in the art to identify other restriction enzymes which can be used to identify a particular polymorphism, for example http://darwin.bio.geneseo.edu which can give restriction enzymes upon analysis of a sequence and the polymorphism to be identified. In fact as disclosed in the teachings herein there are numerous ways of identifying a particular polymorphism or allele with alternate methods which may not even include a restriction enzyme, but which assay for the same genetic or proteomic alternative form.

On page 8, please replace the paragraph at line 22 with the following:

Figure 2 depicts the Polymorphic pattern of AluI digested PCR product. The forward primer 5'-CCC AAA ACA GCA GGA GAA CG-3' (SEQ ID NO:1) and the reverse primer 5'-GGC AAG TGG TTG AAA ATG GA-3' (SEQ ID NO:2) were used in the following PCR conditions: 93°C for 3 minutes, and 35 cycles of 93°C 30 seconds, 60°C 1 minute, 70°C 1 minute, and a final 72°C 3 minutes. The Taq Polymerase was added last while samples were held at 80°C. PCR products were cut with Alu I (New England Biolabs) and separated on a 6% NuSieve (FMC) agarose gel at 120 volts for 4 hours at room temperature. Gels were stained with ethidium bromide. Lane 1 is 1-kb ladder, lanes 2-4 are the three different genotypes.

On page 9, please replace the paragraph at line 5 with the following:

Figure 5 illustrates the sequence (SEQ ID NO:14) surrounding the HinFI site in the intron between exons 8 and 9. Original primers are underlined. Each of the SNP locations are bolded. Additional primer sites designed for analysis are indicated with a line above and below the primers.

On page 9, please replace the paragraph at line 16 with the following:

Figure 9 depicts sequence of porcine introns 3 and 4 and exon 4 which may be used to design alternate primers for the AluI site (SEQ ID NO:15). Exon 4 is bolded, intron 3 precedes the bolded segment and intron 4 follows. Also shown is human exon 4 (SEQ ID NO:16) and an alignment between human (SEQ ID NO:16) and porcine (SEQ ID NO:17) sequences together with porcine sequence for the introns flanking exon 4. This information helps to design alternate primers for these polymorphisms.

On page 17, please replace the paragraph at line 20, under the heading "Denaturing Gradient Gel Electrophoresis" with the following:

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. DNA molecules melt in segments, termed melting domains, under conditions of increased temperature or denaturation. Each melting domain melts cooperatively at a distinct, base-specific melting temperature ~~(TM)~~ (T_m). Melting domains are at least 20 base pairs in length, and may be up to several hundred base pairs in length.

On page 21, please replace the paragraph at line 5, with the following:

Yet another technique includes an Invader Assay which includes isothermic amplification that relies on a catalytic release of fluorescence. See Third Wave Technology at www.twt.com.

On page 23, please replace the paragraph at line 1, with the following:

According to the invention, 4 polymorphisms in the prolactin receptor gene have been identified which have an association with litter size. The presence or absence of the markers, in one embodiment may be assayed by PCR RFLP analysis using the restriction endonuclease AluI, HinFI, MseI, or HpyCH4IV and amplification primers may be designed using analogous human or rabbit or other known prolactin sequences due to the high homology in the region surrounding the polymorphisms, or may be designed using known pig prolactin gene sequence data as exemplified in Figure 1 or even designed from sequences obtained from linkage data from closely surrounding genes based upon the teachings and references herein. The sequences surrounding the polymorphism will facilitate the development of alternate PCR tests in which a primer of about 4-30 contiguous bases taken from the sequence immediately adjacent to the polymorphism is used in connection with a polymerase chain reaction to greatly amplify the region before treatment with the desired restriction enzyme. The primers need not be the exact complement; substantially equivalent sequences are acceptable. According to the invention for the Alu I site a set of primers have been selected which amplify a 457 base pair fragment (forward primer 5'-CCC AAA ACA GCA GGA GAA CG-3' (SEQ ID NO:1) and the reverse primer 5'- GGC AAG TGG TTG AAA ATG GA-3' (SEQ ID NO:2)) after restriction polymorphic fragments of approximately 124, 110, 79, 77, and 67 base pairs are generated. The polymorphic site is located in the 110 base pair fragment. When the polymorphic cut site is

present a 90 base pair fragment is produced. The polymorphic fragments were shown to be alleles, and each was shown to be associated with increased litter size for various breeds. Thus a pig which is heterozygous for the AluI fragment will exhibit a pattern of 124, 110, 90, 79, 77 and 67. A homozygote for the polymorphic cut site will exhibit a ~~patter~~ pattern of 124, 90, 79,77,67, while the other homozygote exhibits a pattern of 124,110, 79,77,67. The genotype associated with larger litter size alternates for different breeds. This outcome is similar to the situation disclosed in U.S. patent 5,374,523 entitled "Allelic variants of Bovine Somatotropin gene: Genetic marker for Superior Milk Production in Bovine" where the inventor found an allelic polymorphism is the somatotropin gene and one allelic form was beneficial for Jersey cows and the alternate form was beneficial for Holstein cows.

On page 24, please replace the paragraph at line 12, with the following:

Another alternate gene form was identified by the inventors which is correlated with litter size and number born alive which is identifiable by a HpyCH4IV digestion. Primers were also identified to optimize a PCR based assay, 5'-GAT TAT TGT CTG GGC AGT GG-3' SEQ ID NO:10 and 5'-~~AATR~~ AAT CCT TTT ATT TTT GGC CC-3' SEQ ID NO:11.

On page 38, please replace the paragraph at line 18, under "Example 7", second paragraph, with the following:

2) A PCR product of approximately 650 bp was amplified using a forward primer (5' GAT TAT TGT CTG GGC AGT GG 3') (SEQ ID NO:10) placed in exon 8 and a reverse primer (5' AAT CCT TTT ~~AT~~ ATT TTT GGC CC 3') (SEQ ID NO:11) located in exon 9 of the prolactin receptor gene. These primers are indicated on the sequence. A 30 µl PCR reaction was prepared

using 3 µl DNA, 1.5 mM MgCl2, 0.2 mM each dNTP, 0.1 µM each primer, 1.5 U TaqGold Polymerase (Applied Biosystems, Foster City, CA) with 1X supplied reaction buffer. Thermal cycling conditions were denaturing at 94°C for 12 min then 40 cycles of 94°C for 1 min, 54°C for 1 min and 72°C for 1 min, following the cycling a final extension at 72°C for 7 min occurred, then products were held at 4°C until removal from the thermal cycler. PCR was performed in a Perkin Elmer 9700 thermal cycler (Applied Biosystems, Foster City, CA).

On page 41, please replace the paragraph at line 2, under "PRLR-HinFi TEST PROTOCOL, with the following:

PRLR(4)-F 5' CAA GGT GGG AAC ATG AGT 3' (SEQ ID NO:8)

PRLR-9R 5' AAT CCT TTT ATT TTT GGC CC 3' (SEQ ID NO:9)

On page 42, please replace the paragraph at line 2, under "PRLR- HpyCH4IV TEST PROTOCOL", with the following:

PRLR-8F 5' GAT TAT TGT CTG GGC AGT GG 3' (SEQ ID NO:10)

PRLR-9R 5' AAT CCT TTT ATT TTT GGC CC 3' (SEQ ID NO:11)

On page 43, please replace the paragraph at line 2, under "PRLR- MseI TEST PROTOCOL", with the following:

PRLR-8F 5' GAT TAT TGT CTG GGC AGT GG 3' (SEQ ID NO:12)

PRLR(2-3)-R 5' CTA TTT CAC AAC TGC GCT AC 3' (SEQ ID NO:13)